

51791AUSC1.ST25.txt
SEQUENCE LISTING

<110> Harkins, Richard
Parkes, Deborah
Parry, Gordon
Schneider, Douglas
Steinbrecher, Renate

<120> DNA Encoding a Novel RG-1 Polypeptide

<130> 51791AUSC1

<150> US 60/172,370

<151> 1999-12-16

<150> US 09/732,357

<151> 2000-12-07

<160> 31

<170> PatentIn version 3.1

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gtcttggtg ggacccgacc gctgccggcc gcgctccgcg tgetcctgcc ggggtg atg 298
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1
gaa aac ccc agc ccg gcc gcc gcc ctg ggc aag gcc ctc tgc gct ctc 346
Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala Leu
5 10 15
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Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu Ser
20 25 30
atc tgt tcc gcc gga gcc ccg gcc aaa tac agc atc acc ttc acg ggc 442
Ile Cys Ser Ala Gly Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr Gly
35 40 45
aag tgg agc cag acg gcc ttc ccc aag cag tac ccc ctg ttc cgc ccc 490

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Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala	Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala		
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Gly	Glu	Ala	Leu	Gln	Ser	Val	His	Ala	Val	Phe	Ser	Ala	Pro	Ala	Val		
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His	Ser	Leu	Val	Ser	Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp		
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 Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu Glu
 310 315 320
 gag gct gag tgc gtc cct gat aac tgc gtc taa gaccagagcc ccgcagcccc 1311
 Glu Ala Glu Cys Val Pro Asp Asn Cys Val
 325 330
 tggggccccc cggagccatg ggggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg 1371
 ccgagggcac aggggggtttc gcgctgctcc tgaccgcggt gaggccgcgc cgaccatctc 1431
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 tccaggagat tgtccttcat cgtccagggg cctggctccc acgtgggtgc agatacctca 1671
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 35 40 45

Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg
 50 55 60

Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp
 65 70 75 80

Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp
 85 90 95

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Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala
 100 105 110

Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala
 115 120 125

Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg
 130 135 140

Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp
 145 150 155 160

Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp
 165 170 175

Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp
 180 185 190

Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp
 195 200 205

Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser
 210 215 220

Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr
 225 230 235 240

Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro
 245 250 255

Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro
 260 265 270

Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu
 275 280 285

Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr
 290 295 300

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19

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15

<210> 5
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<220>
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<210> 13
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 <212> PRT
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<400> 13

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 20 25 30

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 35 40 45

Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg Pro
 50 55 60

Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp Tyr
 65 70 75 80

Ser Met Trp Arg Lys Asn Glu Tyr Val Ser Asn Gly Leu Arg Asp Phe
 85 90 95

Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala
 100 105 110

Gly Glu Lys Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val
 115 120 125

Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val His Pro Arg
 130 135 140

His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp
 145 150 155 160

Phe Val Gly Ile Asp Ser Leu Asp Leu Cys Glu Gly Gly Arg Trp Lys

165

170

175

Glu Gln Val Val Leu Asp Leu Tyr Pro His Asp Ala Gly Thr Asp Ser
 180 185 190

Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr
 195 200 205

Val Thr Glu Ile Thr Ala Ser Ser Pro Ser His Pro Ala Asn Ser Phe
 210 215 220

Tyr Tyr Pro Arg Leu Lys Ser Leu Pro Pro Ile Ala Lys Val Thr Phe
 225 230 235 240

Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ala Pro Pro Ser Leu Asp
 245 250 255

Leu Ala Ser Arg Gly Asn Glu Ile Val Asp Ser Leu Ser Val Pro Glu
 260 265 270

Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys
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Gly Gly Pro Cys Gly Lys Leu Gly Ala Lys Ser Arg Thr Arg Tyr Val
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<213> Homo sapiens

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ctctctctgca gggccagtc gagtggttagc agcagctact tagcctggta ccagcagaaa      180
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      240
gacagggtca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag      300
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tgtgcaggct ctggattcac cttcagtagc tatgttatgc actggcttcg ccaggctcca      180
ggaaaaggtc tggagtgggt atcagttatt ggtactgggt gtgtcacaca ctatgcagac      240
tccgtgaagg gccgattcac catctccaga gacaatgcc aagaactcctt gtatcttcaa      300
atgaacagcc tgagagccga ggacatggct atgtattact gtgcaagatg gggttactat      360
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<210> 22

<211> 441

<212> DNA

<213> Homo sapiens

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tgtgcaggct ctggattcac cttcagtagc tatgttatgc actggcttcg ccaggctcca      180
ggaaaaggtc tggagtgggt atcagttatt ggtactgggt gtgtcacaca ctatgcagac      240
tccgtgaagg gccgattcac catctccaga gacaatgcc aagaactcctt gtatcttcaa      300
atgaacagcc tgagagccga ggacacggct gtgtattact gtgcaagatg gggttactat      360

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<213> Homo sapiens

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ctctctgca gggccagtc gagtggttagc agcagctact tagcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 240

gacaggttca gtggcagtggt gtctgggaca gacttctctc tcaccatcag cagactggag 300

cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcactcac ttccggcgga 360

gggaccaagg tggagatcaa a 381

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<212> DNA

<213> Homo sapiens

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tgtgcaggct ctggattcac cttcagtagc tatgtcatgc actgggttcg ccaggctcca 180

ggaaaaggtc tggagtgggt atcagtaatt ggtactggtg gtgtcacaaa ctatgcagac 240

tccgtgaagg gccgattcac catctccaga gacaatgcca agaactcctt gtatcttcaa 300

atgaacagcc tgagagccga ggacatggct gtgtattact gtgcaagatg gggggactgg 360

gatgatgctt ttgatattct gggccaaggg acaatggta ccgtctcttc agcctccacc 420

aag 423

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<211> 423

<212> DNA

<213> Homo sapiens

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 atgaacagcc tgagagccga ggacacggct gtgtattact gtgcaagatg gggggactgg 360
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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45

Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
 65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
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Ser Ser Ser Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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<400> 27

51791AUSC1.ST25.txt

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20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Val Met His Trp Leu Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Val Ile Gly Thr Gly Gly Val Thr His Tyr Ala Asp
65 70 75 80

Ser Val Lys Gly Arg Phe Met Ile Ser Arg Asp Asn Ala Lys Asn Ser
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Met Tyr
100 105 110

Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Gly Ser Tyr Glu Asn Asp
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Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala
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Ser Thr Lys
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20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe
35 40 45

51791AUSC1.ST25.txt

Ser Ser Tyr Val Met His Trp Leu Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Val Ile Gly Thr Gly Gly Val Thr His Tyr Ala Asp
65 70 75 80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
100 105 110

Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Gly Ser Tyr Glu Asn Asp
115 120 125

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala
130 135 140

Ser Thr Lys
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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

51791AUSC1.ST25.txt

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
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Gly Ser Ser Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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20 25 30

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35 40 45

Ser Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Val Ile Gly Thr Gly Gly Val Thr Asn Tyr Ala Asp
65 70 75 80

Ser Val Lys Gly Arg Phe Met Ile Ser Arg Asp Asn Ala Lys Asn Ser
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
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Tyr Cys Ala Arg Trp Gly Asp Trp Asp Asp Ala Phe Asp Ile Trp Gly
115 120 125

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

<210> 31
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Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe	35	40	45
Ser Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	50	55	60
Glu Trp Val Ser Val Ile Gly Thr Gly Gly Val Thr Asn Tyr Ala Asp	65	70	75
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser	85	90	95
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr	100	105	110
Tyr Cys Ala Arg Trp Gly Asp Trp Asp Asp Ala Phe Asp Ile Trp Gly	115	120	125
Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys	130	135	140